What is claimed is:

1. A method for improving a genetic stability of a foreign insert nucleotide sequence in a recombinant single-stranded RNA virus vector, which comprises performing a mutagenesis of the foreign insert nucleotide sequence to provide even distribution of G/C content throughout the overall foreign DNA sequence.

2. The method according to claim 1, wherein the recombinant single-stranded RNA virus vector is derived from one selected from the group consisting of a poliovirus recombinant vector, a yellow fever virus vector, a Venezuelan equine encephalitis virus vector, a rubella virus vector and a Coxsackie virus vector.

3. A method for improving a genetic stability of a foreign insert nucleotide sequence in a recombinant poliovirus vector, which comprises performing a mutagenesis of the foreign insert nucleotide sequence to provide even distribution of G/C content throughout the overall foreign DNA sequence.

4. The method according to claim 1 or 3, wherein the mutagenesis to provide even distribution of G/C content throughout the overall foreign DNA sequence is performed by increasing G/C content of the foreign DNA sequence.

5. The method according to claim 4, wherein the mutagenesis renders the foreign DNA sequence to have the G/C content of more than 40%.

6. The method according to claim 1 or 3, wherein the mutagenesis of the foreign DNA sequence to provide even distribution of G/C content is performed by increasing G/C content of local A/T-rich region in the foreign DNA sequence.

7. The method according to claim 1 or 3, wherein the mutagenesis is performed by silent mutations.

8. The method according to claim 1 or 3, wherein the foreign DNA sequence is smaller than 450 bp in size.

9. The method according to claim 2 or 3, wherein the recombinant poliovirus vector is one selected from the group consisting of poliovirus type 1, poliovirus type 2 and poliovirus type 3.

10. The method according to claim 2 or 3, wherein the poliovirus is one selected from the group consisting of Sabin type 1, Sabin type 2 and Sabin type 3.

11. The method according to claim 1 or 3, wherein the foreign DNA sequence encodes an antigenic determinant site

of an infectious virus selected from HIV, HCV, HBV, HPV, HSV, rotavirus, influenza virus and epidemic hemorrhagic fever virus.

12. The method according to claim 3, wherein the foreign DNA sequence is inserted into the 5'-end of the recombinant poliovirus vector.

13. The method according to claim 12, wherein the foreign DNA sequence is inserted into a cloning site containing at least one restriction cleavage site artificially formed at the 5'-end of the recombinant poliovirus vector.

14. The method according to claim 13, wherein the cloning site further comprises at its 3'-direction a protease cleavage site recognized by 3C-protease encoded by a poliovirus genome.

15. A method for improving a genetic stability of a foreign insert nucleotide sequence in a recombinant Sabin type 1 poliovirus vector comprising (a) a genomic nucleotide sequence of poliovirus; (b) a cloning site containing restriction cleavage sites artificially formed at the 5'-end of the genomic nucleotide sequence; and (c) a 3C-protease cleavage site formed between the genomic nucleotide sequence and the cloning site, which comprises performing a mutagenesis of the foreign DNA sequence

inserted into the cloning site in order to provide even distribution of G/C content throughout the overall foreign DNA sequence and to have the G/C content of more than 40%.

16. A method for improving a genetic stability of a foreign insert nucleotide sequence in a recombinant Sabin type 1 poliovirus vector comprising (a) a genomic nucleotide sequence of poliovirus; (b) a multiple cloning site containing restriction cleavage sites artificially formed at the 5'-end of the genomic nucleotide sequence; and (c) a 3C-protease cleavage site formed between the genomic nucleotide sequence and the cloning site, which comprises performing a mutagenesis of the foreign DNA sequence which is inserted into the multiple cloning site and encodes a multimeric antigen determinant site containing repeated amino acid sequences in order to provide even distribution of G/C content throughout the overall foreign DNA sequence and to avoid repeated nucleotide sequences by use of degeneracy of genetic code.

17. The method according to claim 16, wherein the mutated foreign DNA sequence encoding multimeric antigen determinant site is prepared by a ligation-free PCR method which comprises the steps of:

(i) preparing a plurality of DNA fragment serving as both template and primer and having the following characteristics: (a) the plural primers are designed

by dividing the entire DNA sequence encoding the multimeric antigen determinant site into several fragments with suitable size; (b) the 5'- and/or 3'-ends of the plural primers comprise a complementary sequence to the terminal sequence of other primer; (c) the complementary sequence is 8-20 mer in size and has G/C content of more than 35%; (d) the primers corresponding to both ends in amplification step have a cloning site containing restriction cleavage site;

(ii) mixing the primers such that the concentration ratio of the primers corresponding to both ends in amplification step to the other primers is 1:3-1:8;

(iii) preparing a full length of the foreign DNA sequence with desired size encoding multimeric antigen determinant site by PCR for 20-40 sec at 92-96℃ (denaturation), for 20-40 sec at 25-40℃ (annealing) and for 30-55 sec at 68-75℃ (extension); and

(iv) amplifying the prepared full length of the foreign DNA sequence by PCR for 20-40 sec at 92-96℃ (denaturation) and 40 sec - 1 min 10 sec at 68-75℃ (annealing and extension).

18. A method for amplifying a DNA sequence using a ligation-free PCR method, which comprises the steps of:

(i) preparing a plurality of DNA fragment serving as both template and primer and having the following characteristics: (a) the plural primers are designed

by dividing the entire DNA sequence of interest into several fragments into several fragments with suitable size; (b) the 5'- and/or 3'-ends of the plural primers comprise a complementary sequence to the terminal sequence of other primer;

(ii) mixing the primers such that the primers corresponding to both ends which is used in amplification step has a higher concentration than the other primers;

(iii) preparing a full length of the foreign DNA sequence with desired size encoding multimeric antigen determinant site by PCR for 20-40 sec at 92-96℃ (denaturation), for 20-40 sec at 25-40℃ (annealing) and for 30-55 sec at 68-75℃ (extension); and

(iv) amplifying the prepared full length of the foreign DNA sequence by PCR for 20-40 sec at 92-96℃ (denaturation) and 40 sec - 1 min 10 sec at 68-75℃ (annealing and extension).

19. The method according to claim 18, wherein the concentration ratio of the primers corresponding to both ends in amplification step to the other primers is 1:3-1:8.

20. The method according to claim 18, wherein the complementary sequence at the the 5'- and/or 3'-ends of the primers is 8-20 mer in size and has G/C content of more than 35%.

21. The method according to claim 18, wherein the primers corresponding to both ends in amplification step have a cloning site containing restriction cleavage site.

22. A recombinant single-stranded RNA virus vector comprising a foreign DNA sequence, characterized in that the foreign DNA sequence is mutated to provide even distribution of G/C content throughout the overall foreign DNA sequence for improving a genetic stability and the recombinant single-stranded RNA virus vector is derived from one selected from the group consisting of a poliovirus recombinant vector, a yellow fever virus vector, a Venezuelan equine encephalitis virus vector, a rubella virus vector and a Coxsackie virus vector.

23. The recombinant single-stranded RNA virus vector according to claim 22, wherein the foreign DNA sequence mutated has the G/C content of more than 40% and is smaller than 450 bp in size.

24. A recombinant poliovirus vector comprising a foreign DNA sequence, characterized in that the foreign DNA sequence is mutated to provide even distribution of G/C content throughout the overall foreign DNA sequence for improving a genetic stability and the recombinant poliovirus vector is derived from one selected from the group consisting of poliovirus type 1, poliovirus type 2

and poliovirus type 3.

25. The recombinant poliovirus vector according to claim 24, wherein the foreign DNA sequence mutated has the G/C content of more than 40%.

26. The recombinant poliovirus vector according to claim 24 or 25, wherein the foreign DNA sequence is smaller than 450 bp in size

27. The recombinant poliovirus vector according to claim 24, wherein the recombinant poliovirus vector is derived from one selected from the group consisting of Sabin type 1, Sabin type 2 and Sabin type 3.

28. The recombinant poliovirus vector according to claim 24, wherein the foreign DNA sequence is inserted into a cloning site containing at least one restriction cleavage site artificially formed at the 5'-end of the recombinant poliovirus vector.

29. The recombinant poliovirus vector according to claim 28, wherein the cloning site further comprises at its 3'-direction a protease cleavage site recognized by 3C-protease encoded by a poliovirus genome.